RAW SEQUENCE LISTING

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Application Serial Number: 10/554,026
Source: PCT/10
Date Processed by STIC: 11/1/05

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RAW SEQUENCE LISTING DATE: 11/01/2005
PATENT APPLICATION: **US/10/554,026** TIME: 10:53:13

Input Set : **A:\Q90951 Sequence Listing.txt**
Output Set: **N:\CRF4\11012005\J554026.raw**

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      3 <110> APPLICANT: Japan Science and Technology Agency
W-->  4 <120> TITLE OF INVENTION: APOPTOSIS-INDUCING AGENT AND METHOD FOR INDUCING APOPTOSIS
W-->  5 <130> FILE REFERENCE: Q90951
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/554,026
C-->  6 <141> CURRENT FILING DATE: 2005-10-21
      6 <150> PRIOR APPLICATION NUMBER: JP 2003-116299
      7 <151> PRIOR FILING DATE: 2003-04-21
W-->  8 <160> NUMBER OF SEQ ID: 14
     10 <170> SOFTWARE: PatentIn version 3.1
     12 <210> SEQ ID NO: 1
     13 <211> LENGTH: 1853
     14 <212> TYPE: DNA
     15 <213> ORGANISM: Homo sapiens
     17 <220> FEATURE:
     18 <221> NAME/KEY: CDS
     19 <222> LOCATION: (65)..(1693)
     21 <300> PUBLICATION INFORMATION:
     22 <301> AUTHORs: Liu, J. et al.
     23 <302> TITLE: Defective interplay of activators with TFIH in xerderma
     24       pigmentosum
     25 <303> JOURNAL: Cell
     26 <304> VOLUME: 104
     27 <305> ISSUE: 3
     28 <306> PAGES: 353-353
     29 <307> DATE: 2001
     30 <308> DATABASE ACCESSION NO: GenBank/NM_14281
     31 <309> DATABASE ENTRY DATE: 2001-12-26
     32 <313> RELEVANT RESIDUES: 1 TO 1853
     34 <400> SEQUENCE: 1
     35 atcgcgcgag acagcggaag gagcaagagt gggaggcgcg cgcggaggcc gcgacggacg 60
     37 caag atg gcg acg gcg acc ata gct ctc cag gtc aat ggc cag caa gga  109
     38      Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly
     39        1               5                  10                  15
     41 ggg ggg tcc gag ccg gcg gcg gcg gcg gca gtg gtg gca gcg gga gac   157
     42 Gly Gly Ser Glu Pro Ala Ala Ala Ala Ala Val Val Ala Ala Gly Asp
     43                  20                  25                  30
     45 aaa tgg aaa cct cca cag ggc aca gac tcc atc aag atg gag aac ggg   205
     46 Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly
     47              35                  40                  45
     49 cag agc aca gcc gcc aag ctg ggg ctg cct ccc ctg acg ccc gag cag   253
     50 Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln
     51          50                  55                  60
     53 cag gag gcc ctt cag aag gcc aag aag tac gcc atg gag cag agc atc   301
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54 Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile
55      65                  70                  75
57 aag agt gtg ctg gtg aag cag acc atc gcg cac cag cag cag cag ctc   349
58 Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu
59  80                  85                  90                  95
61 acc aac ctg cag atg gcg gct cag cgg cag cgg gcg ctg gcc atc atg   397
62 Thr Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met
63                 100                 105                 110
65 tgc cgc gtc tac gtg ggc tct atc tac tat gag ctg ggg gag gac acc   445
66 Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr
67             115                 120                 125
69 atc cgc cag gcc ttt gcc ccc ttt ggc ccc atc aag agc atc gac atg   493
70 Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met
71         130                 135                 140
73 tcc tgg gac tcc gtc acc atg aag cac aag ggc ttt gcc ttc gtg gag   541
74 Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu
75     145                 150                 155
77 tat gag gtc ccc gaa gct gca cag ctg gcc ttg gag cag atg aac tcg   589
78 Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser
79 160                 165                 170                 175
81 gtg atg ctg ggg ggc agg aac atc aag gtg ggc aga ccc agc aac ata   637
82 Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile
83                 180                 185                 190
85 ggg cag gcc cag ccc atc ata gac cag ttg gct gag gag gca cgg gcc   685
86 Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala
87             195                 200                 205
89 ttc aac cgc atc tac gtg gcc tct gtg cac cag gac ctc tca gac gat   733
90 Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp
91         210                 215                 220
93 gac atc aag agc gtg ttt gag gcc ttt ggc aag atc aag tcc tgc aca   781
94 Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr
95     225                 230                 235
97 ctg gcc cgg gac ccc aca act ggc aag cac aag ggc tac ggc ttc att   829
98 Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile
99 240                 245                 250                 255
101 gag tac gag aag gcc cag tcg tcc caa gat gct gtg tct tcc atg aac   877
102 Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn
103                260                 265                 270
105 ctc ttt gac ctg ggt ggc cag tac ttg cgg gtg ggc aag gct gtc aca   925
106 Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr
107            275                 280                 285
109 ccg ccc atg ccc cta ctc aca cca gcc acg cct gga ggc ctc cca cct   973
110 Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro
111        290                 295                 300
113 gcc gct gct gtg gca gct gct gca gcc act gcc aag atc aca gct cag   1021
114 Ala Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln
115     305                 310                 315
117 gaa gca gtg gcc gga gca gcg gtg ctg ggt acc ctg ggc aca cct gga   1069
118 Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly
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119 320                 325                 330                 335
121 ctg gtg tcc cca gca ctg acc ctg gcc cag ccc ctg ggc act ttg ccc  1117
122 Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro
123                 340                 345                 350
125 cag gct gtc atg gct gcc cag gca cct gga gtc atc aca ggt gtg acc  1165
126 Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr
127             355                 360                 365
129 cca gcc cgt cct cct atc ccg gtc acc atc ccc tcg gtg gga gtg gtg  1213
130 Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val
131         370                 375                 380
133 aac ccc atc ctg gcc agc cct cca acg ctg ggt ctc ctg gag ccc aag  1261
134 Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys
135     385                 390                 395
137 aag gag aag gaa gaa gag gag ctg ttt ccc gag tca gag cgg cca gag  1309
138 Lys Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu
139 400                 405                 410                 415
141 atg ctg agc gag cag gag cac atg agc atc tcg ggc agt agc gcc cga  1357
142 Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg
143                 420                 425                 430
145 cac atg gtg atg cag aag ctg ctc cgc aag cag gag tct aca gtg atg  1405
146 His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met
147             435                 440                 445
149 gtt ctg cgc aac atg gtg gac ccc aag gac atc gat gat gac ctg gaa  1453
150 Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu
151         450                 455                 460
153 ggg gag gtg aca gag gag tgt ggc aag ttc ggg gcc gtg aac cgc gtc  1501
154 Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val
155     465                 470                 475
157 atc atc tac caa gag aaa caa ggc gag gag gag gat gca gaa atc att  1549
158 Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile
159 480                 485                 490                 495
161 gtc aag atc ttt gtg gag ttt tcc ata gcc tct gag act cat aag gcc  1597
162 Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala
163                 500                 505                 510
165 atc cag gcc ctc aat ggc cgc tgg ttt gct ggc cgc aag gtg gtg gct  1645
166 Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala
167             515                 520                 525
169 gaa gtg tac gac cag gag cgt ttt gat aac agt gac ctc tct gcg tga  1693
170 Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala
171         530                 535                 540
173 cagtggtccc tctccccgga cttgcacttg ttccttgttt cctctgggtt ttatagtgat 1753
175 acagtggtgt ccccggggcc aggcgcgctc tgcccagccc agcctacagt gcggataaag 1813
177 gtgcggatgc tgctggccct gaaaaaaaaa aaaaaaaaaa                       1853
180 <210> SEQ ID NO: 2
181 <211> LENGTH: 542
182 <212> TYPE: PRT
183 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 2
186 Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln Gln Gly Gly
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187   1               5                  10                  15
188 Gly Ser Glu Pro Ala Ala Ala Ala Ala Val Val Ala Ala Gly Asp Lys
189              20                  25                  30
190 Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu Asn Gly Gln
191          35                  40                  45
192 Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro Glu Gln Gln
193      50                  55                  60
194 Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln Ser Ile Lys
195  65                  70                  75                  80
196 Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln Gln Leu Thr
197                  85                  90                  95
198 Asn Leu Gln Met Ala Ala Gln Arg Gln Arg Ala Leu Ala Ile Met Cys
199             100                 105                 110
200 Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly Glu Asp Thr Ile
201         115                 120                 125
202 Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser Ile Asp Met Ser
203     130                 135                 140
204 Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala Phe Val Glu Tyr
205 145                 150                 155                 160
206 Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln Met Asn Ser Val
207                 165                 170                 175
208 Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro Ser Asn Ile Gly
209             180                 185                 190
210 Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu Ala Arg Ala Phe
211         195                 200                 205
212 Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu Ser Asp Asp Asp
213     210                 215                 220
214 Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys Ser Cys Thr Leu
215 225                 230                 235                 240
216 Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr Gly Phe Ile Glu
217                 245                 250                 255
218 Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser Ser Met Asn Leu
219             260                 265                 270
220 Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys Ala Val Thr Pro
221         275                 280                 285
222 Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly Leu Pro Pro Ala
223     290                 295                 300
224 Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile Thr Ala Gln Glu
225 305                 310                 315                 320
226 Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly Thr Pro Gly Leu
227                 325                 330                 335
228 Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly Thr Leu Pro Gln
229             340                 345                 350
230 Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr Gly Val Thr Pro
231         355                 360                 365
232 Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val Gly Val Val Asn
233     370                 375                 380
234 Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu Glu Pro Lys Lys
235 385                 390                 395                 400
```

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Output Set: N:\CRF4\11012005\J554026.raw

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236 Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu Arg Pro Glu Met
237                 405                 410                 415
238 Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser Ser Ala Arg His
239             420                 425                 430
240 Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser Thr Val Met Val
241         435                 440                 445
242 Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp Asp Leu Glu Gly
243     450                 455                 460
244 Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val Asn Arg Val Ile
245 465                 470                 475                 480
246 Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala Glu Ile Ile Val
247                 485                 490                 495
248 Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr His Lys Ala Ile
249             500                 505                 510
250 Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys Val Val Ala Glu
251         515                 520                 525
252 Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu Ser Ala
253     530                 535                 540
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 18
257 <212> TYPE: DNA
258 <213> ORGANISM: Artificial Sequence
260 <220> FEATURE:
261 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
W--> 262 <400> SEQUENCE: 3
263 ggccccatca agagcatg                                              18
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 19
267 <212> TYPE: DNA
268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
W--> 272 <400> SEQUENCE: 4
273 ggggctgggc cagggtcag                                             19
275 <210> SEQ ID NO: 5
276 <211> LENGTH: 18
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence
280 <220> FEATURE:
281 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
W--> 282 <400> SEQUENCE: 5
283 gcacctggag tcatcaca                                              18
285 <210> SEQ ID NO: 6
286 <211> LENGTH: 19
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Artificial Sequence: synthetic DNA
293 <400> SEQUENCE: 6
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VERIFICATION SUMMARY DATE: 11/01/2005
PATENT APPLICATION: **US/10/554,026** TIME: 10:53:14

Input Set : **A:\Q90951 Sequence Listing.txt**
Output Set: **N:\CRF4\11012005\J554026.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8 M:283 W: Missing Blank Line separator, <160> field identifier
L:262 M:283 W: Missing Blank Line separator, <400> field identifier
L:272 M:283 W: Missing Blank Line separator, <400> field identifier
L:282 M:283 W: Missing Blank Line separator, <400> field identifier